SEQUENCE LISTING

<110> St. Boniface General Hospital Research Centre
Mesaeli, Nasrin

<120> Transgenic Mouse over-expressing calreticulin (CRT) in vascular
smooth muscle cells

<130> 81190-2602

<150> US 60/455399
<151> 2003-03-18

<160> 24

<170> PatentIn version 3.2

<210> 1
<211> 2655
<212> DNA
<213> Artificial

<220>
<223> artificial construct of sm22a promoter and CRT cDNA

<220>
<221> CDS
<222> (1319)..(2653)
<223> CRT coding sequence

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tcctgggtga gactgaccct gcctgagggt tctctccttc cctctctcta ctcctttcct   180

ccctctccct ctccctctct ctgtttcctg aggtttccag gattgggat gggactcaga   240

gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca   300

cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac   360

tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg   420

tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt   480

aggatctttc acgataagga ctattttgaa gggaggagg gtgacactgt cctagtcctc   540

ttaccctagt gtcctccagc cttgccaggc cttaaacatc cgcccattgt caccgctcta   600

gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga   660

agcataccat acctgtgggc aggatgaccc atgttctgcc acgcacttgg tagccttgga   720

aaggccactt tgaacctcaa ttttctcaac tgttaaatgg ggtggtaact gctatctcat   780

aataaagggg aacgtgaaag gaaggcgttt gcatagtgcc tggttgtgca gccaggctgc   840

agtcaagact agttcccacc aactcgattt taaagccttg caagaaggtg gcttgtttgt   900

cccttgcagg ttcctttgtc gggccaaact ctagaatgcc tcccccttc tttctcattg   960

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aagagcagac ccaagtccgg gtaacaagga agggtttcag ggtcctgccc ataaaaggtt    1020

tttcccggcc gccctcagca ccgccccgcc ccgaccccccg cagcatctcc aaagcatgca    1080

gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg    1140

gagcctgtgt ggagtgagtg gggcggcccg gggtggtgag ccaagcagac ttccatgggc    1200

agggaggggc gccagcggac ggcagagggg tgacatcact gcctaggcgg cctttaaacc    1260

cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc      1318
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atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc    1366
Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1               5                   10                  15

gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg    1414
Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
                20                  25                  30

tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa    1462
Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
        35                  40                  45

ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa    1510
Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
    50                  55                  60

ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tcg gcc cga    1558
Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65                  70                  75                  80

ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc    1606
Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
                85                  90                  95

agg acg ccc gct tct acg ccc tgt cgg ccc gat tcg agc cgt tca gca    1654
Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
            100                 105                 110

aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg agc aga    1702
Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro     Asn Thr Ser Arg
        115                 120                 125

aca ttg act gcg ggg gcg gct acg tga agc tgt ttc cgg ccg gcc tgg    1750
Thr Leu Thr Ala Gly Ala Ala Thr     Ser Cys Phe Arg Pro Ala Trp
        130                 135                 140

acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc    1798
Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val
        145                 150                 155

ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act    1846
Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr
        160                 165                 170

aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg    1894
Thr Arg Ala Arg Thr Cys     Ser Thr Arg Thr Ser Val Ala Arg Thr
175                 180                 185

acg agt tca cac acc tgt aca cgc tga tcg tgc ggc cgg aca aca cgt    1942
Thr Ser Ser His Thr Cys Thr Arg     Ser Cys Gly Arg Thr Thr Arg
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190                     195                    200

atg agg tga aga ttg aca aca gcc agg tgg agt cgg gct ccc tgg agg     1990
Met Arg     Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg
205                     210                    215

atg act ggg act tcc tac ccc cca aga aga taa agg acc cag atg cct     2038
Met Thr Gly Thr Ser Tyr Pro Pro Arg Arg     Arg Thr Gln Met Pro
220                     225                    230

cga agc ctg aag act ggg acg agc ggg cca aga tcg acg acc cca cgg     2086
Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg Ser Thr Thr Pro Arg
235                     240                    245                250

act cca agc ccg agg act ggg aca agc ccg agc aca tcc ccg acc cgg     2134
Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser Thr Ser Pro Thr Arg
                        255                    260                265

acg cga aga agc ccg aag act ggg acg aag aaa tgg acg gag agt ggg     2182
Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys Trp Thr Glu Ser Gly
                270                    275                    280

agc cgc cgg tga ttc aga acc ccg agt aca agg gtg agt gga agc cgc     2230
Ser Arg Arg     Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg
                285                    290                    295

ggc aga tcg aca acc ccg att aca aag gca cct gga tcc acc ccg aaa     2278
Gly Arg Ser Thr Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys
                300                    305                    310

tcg aca acc ccg agt act cgc ccg acg cta aca tct atg cct acg aca     2326
Ser Thr Thr Pro Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr
                315                    320                    325

gct ttg ccg tgc tgg gct tgg acc tct ggc agg tca agt cgg gca cca     2374
Ala Leu Pro Cys Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro
330                     335                    340                345

tct tcg aca act tcc tca tca cca acg atg agg cgt acg cag agg agt     2422
Ser Ser Thr Thr Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser
                350                    355                    360

ttg gca acg aga cgt ggg gcg tca cca aga cgg ccg aga agc aga tga     2470
Leu Ala Thr Arg Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
                365                    370                    375

aag aca agc agg acg agg agc agc gga tga agg agg agg agg agg aga     2518
Lys Thr Ser Arg Thr Arg Ser Ser Gly     Arg Arg Arg Arg Arg Arg
                380                    385                    390

aga agc gga agg agg agg agg agg ccg agg agg acg agg agg aca agg     2566
Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg Arg Thr Arg Arg Thr Arg
                395                    400                    405

acg aca agg agg acg agg atg agg acg agg agg aca agg acg agg agg     2614
Thr Thr Arg Arg Thr Arg Met Arg Thr Arg Arg Thr Arg Thr Arg Arg
                410                    415                    420

agg agg agg cgg ccg ccg gcc agg cca agg acg agc tgt ag              2655
Arg Arg Arg Arg Pro Pro Ala Arg Pro Arg Thr Ser Cys
                425                    430                    435
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<210> 2
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<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 2

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1   5   10   15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
            20   25   30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
            35   40   45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
        50   55   60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65   70   75   80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
                85   90   95

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
            100   105   110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro
            115   120

<210> 3
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<220>
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<400> 3

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr
1   5   10

<210> 4
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<213> Artificial

<220>
<223> Synthetic Construct

<400> 4

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu
1   5   10   15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg
            20   25   30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys
        35   40   45

<210> 5
<211> 17
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 5

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr
1   5   10   15

Arg

<210> 6
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 6

Ser Cys Gly Arg Thr Thr Arg Met Arg
1   5

<210> 7
<211> 23
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 7

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly
1   5   10   15

Thr Ser Tyr Pro Pro Arg Arg
            20

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<210>   8
<211>   56
<212>   PRT
<213>   Artificial

<220>
<223>   Synthetic Construct

<400>   8
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Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg
1   5   10   15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser
                20   25   30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys
            35   40   45

Trp Thr Glu Ser Gly Ser Arg Arg
        50   55

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<210>   9
<211>   91
<212>   PRT
<213>   Artificial

<220>
<223>   Synthetic Construct

<400>   9
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Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr
1   5   10   15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro
                20   25   30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys
            35   40   45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr
        50   55   60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg
65   70   75   80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
                85   90

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<210>   10
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<211>  9
<212>  PRT
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<220>
<223>  Synthetic Construct

<400>  10

Lys Thr Ser Arg Thr Arg Ser Ser Gly
1               5


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<211>  51
<212>  PRT
<213>  Artificial

<220>
<223>  Synthetic Construct

<400>  11

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg
1               5                   10                  15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg
            20                  25                  30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Arg Pro Arg
        35                  40                  45

Thr Ser Cys
    50


<210>  12
<211>  2691
<212>  DNA
<213>  Artificial

<220>
<223>  construct of SM22a promoter and CRT cDNA with HA tag inserted
       into CRT cDNA


<220>
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<222>  (1319)..(2689)

<220>
<221>  misc_feature
<222>  (2635)..(2670)
<223>  HA insertion

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gccaggctgg ctgtagtgga ttgagcgtct gaggctgcac ctctctggcc tgcagccagt     120
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crt sequences.ST25

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tcctgggtga gactgaccct gcctgagggt tctctccttc cctctctcta ctcctttcct        180

ccctctccct ctccctctct ctgtttcctg aggtttccag gattgggggat gggactcaga       240

gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca        300

cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac        360

tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg        420

tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt        480

aggatctttc acgataagga ctattttgaa gggagggagg gtgacactgt cctagtcctc        540

ttaccctagt gtcctccagc cttgccaggc cttaaacatc cgcccattgt caccgctcta        600

gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga        660

agcataccat acctgtgggc aggatgaccc atgttctgcc acgcacttgg tagccttgga        720

aaggccactt tgaacctcaa ttttctcaac tgttaaatgg ggtggtaact gctatctcat        780

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cccttgcagg ttcctttgtc gggccaaact ctagaatgcc tcccccttc tttctcattg        960

aagagcagac ccaagtccgg gtaacaagga agggtttcag ggtcctgccc ataaaaggtt       1020

tttcccggcc gccctcagca ccgccccgcc ccgacccccg cagcatctcc aaagcatgca       1080

gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg       1140

gagcctgtgt ggagtgagtg gggcggcccg gggtggtgag ccaagcagac ttccatgggc       1200

agggaggggc gccagcggac ggcagagggg tgacatcact gcctaggcgg cctttaaacc       1260

cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc        1318
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atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc        1366
Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1               5                   10                  15

gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg        1414
Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
                20                  25                  30

tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa        1462
Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
            35                  40                  45

ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa        1510
Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
        50                  55                  60

ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tcg gcc cga        1558
Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65                  70                  75                  80

ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc        1606
Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
                85                  90                  95
```

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agg acg ccc gct tct acg ccc tgt cgg ccc gat tcg agc cgt tca gca    1654
Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
            100                 105                 110

aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg agc aga    1702
Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro     Asn Thr Ser Arg
            115                 120                 125

aca ttg act gcg ggg gcg gct acg tga agc tgt ttc cgg ccg gcc tgg    1750
Thr Leu Thr Ala Gly Ala Ala Thr     Ser Cys Phe Arg Pro Ala Trp
            130                 135                 140

acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc    1798
Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val
            145                 150                 155

ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act    1846
Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr
            160                 165                 170

aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg    1894
Thr Arg Ala Arg Thr Cys     Ser Thr Arg Thr Ser Val Ala Arg Thr
175             180                 185

acg agt tca cac acc tgt aca cgc tga tcg tgc ggc cgg aca aca cgt    1942
Thr Ser Ser His Thr Cys Thr Arg     Ser Cys Gly Arg Thr Thr Arg
190             195                 200

atg agg tga aga ttg aca aca gcc agg tgg agt cgg gct ccc tgg agg    1990
Met Arg     Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg
205             210                 215

atg act ggg act tcc tac ccc cca aga aga taa agg acc cag atg cct    2038
Met Thr Gly Thr Ser Tyr Pro Pro Arg Arg     Arg Thr Gln Met Pro
220             225                 230

cga agc ctg aag act ggg acg agc ggg cca aga tcg acg acc cca cgg    2086
Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg Ser Thr Thr Pro Arg
235             240                 245                 250

act cca agc ccg agg act ggg aca agc ccg agc aca tcc ccg acc cgg    2134
Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser Thr Ser Pro Thr Arg
            255                 260                 265

acg cga aga agc ccg aag act ggg acg aag aaa tgg acg gag agt ggg    2182
Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys Trp Thr Glu Ser Gly
            270                 275                 280

agc cgc cgg tga ttc aga acc ccg agt aca agg gtg agt gga agc cgc    2230
Ser Arg Arg     Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg
            285                 290                 295

ggc aga tcg aca acc ccg att aca aag gca cct gga tcc acc ccg aaa    2278
Gly Arg Ser Thr Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys
            300                 305                 310

tcg aca acc ccg agt act cgc ccg acg cta aca tct atg cct acg aca    2326
Ser Thr Thr Pro Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr
            315                 320                 325

gct ttg ccg tgc tgg gct tgg acc tct ggc agg tca agt cgg gca cca    2374
Ala Leu Pro Cys Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro
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         330                   335                   340                   345

tct tcg aca act tcc tca tca cca acg atg agg cgt acg cag agg agt    2422
Ser Ser Thr Thr Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser
                350                   355                   360

ttg gca acg aga cgt ggg gcg tca cca aga cgg ccg aga agc aga tga    2470
Leu Ala Thr Arg Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
                365                   370                   375

aag aca agc agg acg agg agc agc gga tga agg agg agg agg agg aga    2518
Lys Thr Ser Arg Thr Arg Ser Ser Gly     Arg Arg Arg Arg Arg Arg
                380                   385                   390

aga agc gga agg agg agg agg agg ccg agg agg acg agg agg aca agg    2566
Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg Arg Thr Arg Arg Thr Arg
                395                   400                   405

acg aca agg agg acg agg atg agg acg agg agg aca agg acg agg agg    2614
Thr Thr Arg Arg Thr Arg Met Arg Thr Arg Arg Thr Arg Thr Arg Arg
                410                   415                   420

agg agg agg cgg ccg ccg gcc tcg agt acc cat atg atg ttc ctg act    2662
Arg Arg Arg Arg Pro Pro Ala Ser Ser Thr His Met Met Phe Leu Thr
                425                   430                   435

atg cta gac agg cca agg acg agc tgt ag                             2691
Met Leu Asp Arg Pro Arg Thr Ser Cys
440                   445
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<210>  13
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<212>  PRT
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<220>
<223>  Synthetic Construct

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Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1               5                   10                  15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
                20                  25                  30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
            35                  40                  45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
        50                  55                  60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65                  70                  75                  80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
                85                  90                  95
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Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
            100   105   110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro
        115   120

<210>   14
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<212>   PRT
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<220>
<223>   Synthetic Construct

<400>   14

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr
1   5   10

<210>   15
<211>   45
<212>   PRT
<213>   Artificial

<220>
<223>   Synthetic Construct

<400>   15

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu
1   5   10   15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg
            20   25   30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys
        35   40   45

<210>   16
<211>   17
<212>   PRT
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<220>
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<400>   16

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr
1   5   10   15

Arg

<210> 17
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<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 17

Ser Cys Gly Arg Thr Thr Arg Met Arg
1   5

<210> 18
<211> 23
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<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly
1   5   10   15

Thr Ser Tyr Pro Pro Arg Arg
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<210> 19
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<220>
<223> Synthetic Construct

<400> 19

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg
1   5   10   15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser
            20   25   30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys
        35   40   45

Trp Thr Glu Ser Gly Ser Arg Arg
    50   55

<210> 20
<211> 91
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 20

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr
1   5   10   15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro
            20   25   30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys
        35   40   45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr
    50   55   60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg
65   70   75   80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
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<210> 21
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<212> PRT
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<220>
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<400> 21

Lys Thr Ser Arg Thr Arg Ser Ser Gly
1   5

<210> 22
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<220>
<223> Synthetic Construct

<400> 22

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg
1   5   10   15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg
            20   25   30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Ser Ser Thr
Page 13

His Met Met Phe Leu Thr Met Leu Asp Arg Pro Arg Thr Ser Cys
     50   55   60

<210> 23
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<212> PRT
<213> Artificial

<220>
<223> CRT peptide sequence from CRT cDNA

<400> 23

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1   5   10   15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
      20   25   30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
      35   40   45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
      50   55   60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65   70   75   80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr
          85   90   95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
          100   105   110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr
          115   120   125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
      130   135   140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
145   150   155   160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
          165   170   175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
          180   185   190

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
        195   200   205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
    210   215   220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225   230   235   240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
            245   250   255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
            260   265   270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
        275   280   285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn
    290   295   300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln
305   310   315   320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
            325   330   335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr
            340   345   350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
        355   360   365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu
    370   375   380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu
385   390   395   400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Gln Ala Lys Asp
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Glu Leu

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<220>
<223>  CRT peptide sequence with HA tag inserted into peptide


<220>
<221>  MISC_FEATURE
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<223>  HA Tag

<400>  24
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Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
            20   25   30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
        35   40   45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
    50   55   60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65   70   75   80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr
                85   90   95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
            100   105   110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr
        115   120   125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
    130   135   140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
145   150   155   160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
                165   170   175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
            180   185   190

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Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
        195             200             205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
    210             215             220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225             230             235             240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
            245             250             255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
            260             265             270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
        275             280             285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn
    290             295             300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln
305             310             315             320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
            325             330             335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr
            340             345             350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
        355             360             365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu
    370             375             380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu
385             390             395             400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Leu Glu Tyr Pro
            405             410             415

Tyr Asp Val Pro Asp Tyr Ala Arg Gln Ala Lys Asp Glu Leu
            420             425             430
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